

SCORE Search Results Details for Application 09391861 and Search Result 20070925_081037_us-09-391-861-5.rag.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 09391861 and Search Result 20070925_081037_us-09-391-861-5.rag.

[Go Back to previous page](#)

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 25, 2007, 08:11:41 ; Search time 62 Seconds
(without alignments)
1440.152 Million cell updates/sec

Title: US-09-391-861-5
Perfect score: 969
Sequence: 1 HPIPDSSPLLQFGGQVRQRY.....SSDPLSMVGPSQGRSPSYAS 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	969	100.0	181	4	AAU00965
2	969	100.0	209	4	AAB82351
3	969	100.0	209	4	AAU00957
4	969	100.0	209	4	AAB83951
5	961	99.2	181	9	AEB19074
6	959	99.0	181	9	AEB19069
7	959	99.0	181	9	AEB55174
8	959	99.0	181	9	AED28265
9	959	99.0	181	9	AEE39711
10	959	99.0	181	10	AEG40944
11	959	99.0	181	10	AEG36157
12	959	99.0	181	10	AEI54357
13	959	99.0	181	10	AEJ43843
14	959	99.0	182	10	AEH50993
15	959	99.0	208	4	AAE05078
16	959	99.0	208	5	AAU83630
17	959	99.0	208	5	ABG32358
18	959	99.0	208	5	AAE17601
19	959	99.0	208	5	ADY31818
20	959	99.0	208	6	ABU80777
21	959	99.0	208	6	ABO33743
22	959	99.0	208	6	ABU82086
23	959	99.0	208	6	ABP96156
24	959	99.0	208	6	ABJ72266
25	959	99.0	208	6	ABJ72394
26	959	99.0	208	6	ABO34289
27	959	99.0	208	7	ADA37038
28	959	99.0	208	7	ABJ72096
29	959	99.0	208	7	ADB83568
30	959	99.0	208	7	ADB80674
31	959	99.0	208	7	ADB73215
32	959	99.0	208	7	ADB78297
33	959	99.0	208	7	ADB84945
34	959	99.0	208	7	ADB78051
35	959	99.0	208	7	ADB87117
36	959	99.0	208	7	ADB84699
37	959	99.0	208	7	ADB83814
38	959	99.0	208	7	ADB72969
39	959	99.0	208	7	ADC36807
40	959	99.0	208	7	ADC21797
41	959	99.0	208	7	ADC49828
42	959	99.0	208	7	ADC49027
43	959	99.0	208	7	ADC49544
44	959	99.0	208	7	ADC47405
45	959	99.0	208	7	ADC47150

ALIGNMENTS

RESULT 1

AAU00965

ID AAU00965 standard; protein; 181 AA.

XX

AC AAU00965;

XX
DT 24-MAY-2001 (first entry)
XX
DE Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment.
XX
KW Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;
KW renal tubule damage; gastrointestinal abnormality; wasting syndrome;
KW neurodegenerative disease; haematopoietic cell reconstitution; cachexia;
KW chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;
KW multiple sclerosis; short stature; delayed maturation; excessive growth;
KW acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;
KW androgen target organ abnormality; respiratory distress syndrome; stroke;
KW cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness;
KW osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;
KW decreased stamina; decreased cardiac function; immune system dysfunction;
KW Parkinson's disease; Alzheimer's disease; decreased cognitive function;
KW senile dementia; human.
XX
OS Homo sapiens.
XX
PN WO200118172-A2.
XX
PD 15-MAR-2001.
XX
PF 05-SEP-2000; 2000WO-US024373.
XX
PR 07-SEP-1999; 99US-00391861.
PR 23-AUG-2000; 2000US-00644052.
XX
PA (AMGE-) AMGEN INC.
XX
PI Thomason AR, Liu B;
XX
DR WPI; 2001-226743/23.
XX
PT Novel isolated fibroblast growth factor-like polypeptide useful for
PT treating, preventing or ameliorating cirrhosis, inflammatory bowel
PT disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
PT osteoporosis.
XX
PS Claim 14; Page 116-117; 138pp; English.
XX
CC The sequence represents a fragment of a fibroblast growth factor-like
CC (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid
CC play a role in modulating body growth, maturation or life-span. They are
CC also useful for treating, preventing or ameliorating disorders such as
CC cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease,
CC diabetes, obesity, gastrointestinal abnormalities, neurodegenerative
CC diseases, damage to renal tubules as a result of acute tubular necrosis,
CC haematopoietic cell reconstitution following chemotherapy, wasting
CC syndromes (e.g., cancer associated cachexia), damage to the corneal
CC epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
CC stature, delayed maturation, excessive growth (e.g. acromegaly),
CC premature maturation, alopecia, abnormalities of androgen target organs,
CC bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours
CC of the eye or other tissues, atherosclerosis, hypercholesterolemia,
CC stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia,
CC baldness, wrinkles, increased fatigue, decreased stamina, decreased
CC cardiac function, immune system dysfunction, cancer, Parkinson's disease,
CC senile dementia, Alzheimer's disease, and decreased cognitive function

XX

SQ Sequence 181 AA;

Query Match 100.0%; Score 969; DB 4; Length 181;
 Best Local Similarity 100.0%; Pred. No. 3.7e-76;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 HPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKP 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 HPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKP 60

Qy     61 GVIQILGVKTSRFLCQRPDGLYGLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GVIQILGVKTSRFLCQRPDGLYGLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 120

Qy    121 NKSPHRDPAPRGPARFLPLPGLPPAPPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYA 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 NKSPHRDPAPRGPARFLPLPGLPPAPPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYA 180

Qy    181 S 181
      |
Db    181 S 181

```

RESULT 2

AAB82351

ID AAB82351 standard; protein; 209 AA.

XX

AC AAB82351;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human JAFFA protein.

XX

KW JAFFA; human; fibroblast growth factor; diagnosis; therapy; cancer;

KW autoimmune disease; cytostatic; immunosuppressive; neuroprotective.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .28

FT /label= Signal_peptide

FT Modified-site 6. .9

FT /note= "predicted casein kinase II phosphorylation site"

FT Modified-site 12. .17

FT /note= "N-myristoylation"

FT Modified-site 20. .25

FT /note= "N-myristoylation"

FT Protein 29. .209

FT /label= Mature_protein

FT Domain 60. .140

FT /note= "fibroblast growth factor domain"

FT Modified-site 67. .72

FT /note= "N-myristoylation"

FT Modified-site 95. .100

FT /note= "N-myristoylation"

FT Modified-site 98. .100

FT /note= "protein kinase C predicted phosphorylation site"

FT Modified-site 108. .113

FT /note= "N-myristoylation"

FT Modified-site 122. .125

FT /note= "predicted casein kinase II phosphorylation site"
 FT Modified-site 122. .124
 FT /note= "protein kinase C predicted phosphorylation site"
 XX
 PN WO200138357-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032181.
 XX
 PR 22-NOV-1999; 99US-00444165.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Khodadoust MM;
 XX
 DR WPI; 2001-355881/37.
 DR N-PSDB; AAF90326, AAF90327.
 XX
 PT Isolated JAFFA nucleic acid molecules which encode novel fibroblast
 PT growth factor family members (JAFFA) are useful for developing novel
 PT diagnostic and therapeutic agents for JAFFA-associated disorders such as
 PT cancers.
 XX
 PS Claim 2; Fig 1; 137pp; English.
 XX
 CC The present sequence is that of human JAFFA, a novel member of the
 CC fibroblast growth factor family. Analysis of rare sequences in the
 CC Millennium database led to the identification of an expressed sequence
 CC tag from a human prostate tumour library which coded for a novel
 CC hypothetical signal peptide. Further analysis led to the identification
 CC of JAFFA. The invention provides JAFFA polypeptides, polynucleotides and
 CC anti-JAFFA antibodies. It also provides antisense nucleic acid molecules,
 CC recombinant expression vectors, host cells and transgenic animals. JAFFA
 CC proteins may be useful for developing novel diagnostic and therapeutic
 CC agents for JAFFA-associated disorders such as cancers and other disorders
 CC which demonstrate ABO(H) blood group disorders and for controlling
 CC cellular proliferative and/or differentiative disorders. The JAFFA
 CC nucleic acid and protein may be used to treat and/or diagnose a variety
 CC of immune disorders such as autoimmune disease and multiple sclerosis.
 CC The proteins may also be used to screen for naturally occurring JAFFA
 CC substrates, to screen for drugs or compounds which modulate JAFFA
 CC activity, and to raise anti-JAFFA antibodies, which can be used to detect
 CC and isolate JAFFA proteins, regulate the bioavailability of JAFFA
 CC proteins and modulate JAFFA activity
 XX
 SQ Sequence 209 AA;

Query Match 100.0%; Score 969; DB 4; Length 209;
 Best Local Similarity 100.0%; Pred. No. 4.4e-76;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDDGTGGAADQSPESLLQLKALKP 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 29 HPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDDGTGGAADQSPESLLQLKALKP 88
 Qy 61 GVIQILGVKTSRFLCQRPDGAlyGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 89 GVIQILGVKTSRFLCQRPDGAlyGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 148
 Qy 121 NKSPHRDPAPRGPAPFLPLPGLPPAPPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYA 180